

## Davis, Minh-Tam

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**From:** Davis, Minh-Tam  
**Sent:** Monday, January 09, 2006 4:08 PM  
**To:** Chan, Christina  
**Subject:** Rush search request for 10/048046

1) Please search in commercial database, issued patent files and PGPUB:

A nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.

2) Interference search only for:

- a) SEQ ID NO:1
- b) oligonucleotide search for SEQ ID NO:1, with size limitation for the sequences in the database to equal or less than 50 nucleotides.
- c) A nucleic acid encoding SEQ ID NO:2.
- d) oligonucleotide search for a nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.

Thank you.

MINH TAM DAVIS  
ART UNIT 1642, ROOM 3A24, MB 3C18  
272-0830

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 12, 2006, 07:58:47 / Search time 316 Seconds

(without alignments)  
3735.130 Million cell updates/sec

Title: US-10-048-046-2

Perfect score: 664

Sequences: 1 MERPREKSGSPPOPMGRLL.....VKAHAKMKFNHCCEOTRFKN 664

Scoring table:

Xgapop 60.0	Xgapext 60.0
Ygapop 60.0	Ygapext 60.0
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1293591

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame\_plus.model -DEV=rlh  
-O=/cg2\_1/USPTO\_spool/US10048046/runat\_10012006\_122939\_24142/app\_query.fasta\_1.839  
-DB=Issued\_Patents\_NA -QFMT=fasta -SUPFIX=014g\_sz50.rn1 -MINMATCH=0.1  
-LOOPEL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=0119g  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50  
-USER=US10048046 -CGEN\_1\_1\_193 -runat\_10012006\_122939\_24142 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBIOCK=100 -LONGLIOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Issued\_Patents\_NA:  
1: /cg2\_6/prodata/1/lna/1/COMB.seq:\*  
2: /cg2\_6/prodata/1/lna/5/COMB.seq:\*  
3: /cg2\_6/prodata/1/lna/6A/COMB.seq:\*  
4: /cg2\_6/prodata/1/lna/6B/COMB.seq:\*  
5: /cg2\_6/prodata/1/lna/H/COMB.seq:\*  
6: /cg2\_6/prodata/1/lna/ECTUS/COMB.seq:\*  
7: /cg2\_6/prodata/1/lna/PP/COMB.seq:\*  
8: /cg2\_6/prodata/1/lna/RB/COMB.seq:\*  
9: /cg2\_6/prodata/1/lna/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.1	25	US-09-396-196G-104092	Sequence 104092,
2	7	1.1	25	US-09-396-196G-104100	Sequence 104100,
3	7	1.1	25	US-09-396-196G-104101	Sequence 104101,
4	7	1.1	25	US-09-396-196G-104102	Sequence 104102,
5	7	1.1	25	US-09-396-196G-104103	Sequence 104103,
6	7	1.1	30	US-08-078-683A-35	Sequence 35, Appl
7	7	1.1	30	US-08-471-970A-35	Sequence 35, Appl
8	7	1.1	30	US-09-723-677B-35	Sequence 35, Appl
9	7	1.1	33	US-08-196-538-16	Sequence 16, Appl

10	7	1.1	35	US-08-582-740-6	Sequence 6, Appl1
11	7	1.1	35	US-09-109-879-6	Sequence 63, Appl1
12	7	1.1	39	US-08-582-740-63	Sequence 63, Appl1
13	7	1.1	39	US-09-109-879-63	Sequence 77, Appl1
14	7	1.1	40	US-07-931-473B-77	Sequence 109, Appl
15	7	1.1	40	US-07-931-473B-109	Sequence 109, Appl
16	7	1.1	40	US-07-714-131C-77	Sequence 109, Appl
17	7	1.1	40	US-07-714-131C-109	Sequence 109, Appl
18	7	1.1	40	US-08-412-110-77	Sequence 77, Appl
19	7	1.1	40	US-08-412-110-109	Sequence 109, Appl
20	7	1.1	40	US-08-409-442A-77	Sequence 77, Appl
21	7	1.1	40	US-08-409-442A-109	Sequence 109, Appl
22	7	1.1	40	US-08-469-609A-77	Sequence 77, Appl
23	7	1.1	40	US-08-469-609A-109	Sequence 109, Appl
24	7	1.1	40	US-09-143-190-77	Sequence 77, Appl
25	7	1.1	40	US-09-143-190-109	Sequence 109, Appl
26	7	1.1	40	US-09-502-344-77	Sequence 77, Appl
27	7	1.1	40	US-09-502-344-109	Sequence 109, Appl
28	7	1.1	40	US-10-037-986-77	Sequence 77, Appl
29	7	1.1	40	US-10-037-986-109	Sequence 109, Appl
30	7	1.1	50	US-09-849-069-15	Sequence 15, Appl
31	7	1.1	50	US-10-131-827-5520	Sequence 5920, Ap
32	6	0.9	18	US-08-311-486C-1074	Sequence 1074, Ap
33	6	0.9	18	US-08-311-486C-1141	Sequence 1141, Ap
34	6	0.9	18	US-09-422-978-10937	Sequence 10937, A
35	6	0.9	18	US-10-620-049-3	Sequence 3, Appl1
36	6	0.9	19	US-09-352-654A-31	Sequence 31, Appl1
37	6	0.9	19	US-09-348-097-31	Sequence 31, Appl1
38	6	0.9	19	US-09-350-275-31	Sequence 31, Appl1
39	6	0.9	19	US-09-909-558-31	Sequence 31, Appl1
40	6	0.9	20	US-08-770-565-3	Sequence 3, Appl1
41	6	0.9	20	US-08-964-725-12	Sequence 12, Appl1
42	6	0.9	20	US-08-833-377-7	Sequence 7, Appl1
43	6	0.9	20	US-08-281-203-3	Sequence 3, Appl1
44	6	0.9	20	US-09-166-186-25	Sequence 25, Appl1
45	6	0.9	20	US-09-313-932-25	Sequence 25, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-396-196G-104092/c  
Sequence 104092, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 104092  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-104092

#### Alignment Scores:

Pred. No.: 148  
Score: 7.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 1.05%  
DB: 3  
Gaps: 0  
Length: 25  
Matches: 7  
Mismatch: 0  
Indels: 0

US-10-048-046-2 (1-664) x US-09-396-196G-104092 (1-25)

OY 18 ArgLeuLeuArgLeuGlyAla 24  
 DB 25 AGATTGCTCAGATTGGCGCT 5

RESULT 2  
 US-09-396-196G-104100/c  
 / Sequence 104100, Application US/09396196G  
 / Patent No. 6821724

GENERAL INFORMATION:  
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 104100

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-104100

Alignment Scores:  
 Pred. No.: 148 Length: 25  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-396-196G-104100 (1-25)

OY 18 ArgLeuLeuArgLeuGlyAla 24  
 DB 24 AGATTGCTCAGATTGGCGCT 4

RESULT 3

US-09-396-196G-104101/c

/ Sequence 104101, Application US/09396196G

/ Patent No. 6821724

GENERAL INFORMATION:  
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 104101

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-104101

Alignment Scores:  
 Pred. No.: 148 Length: 25  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-396-196G-104101 (1-25)

OY 18 ArgLeuLeuArgLeuGlyAla 24  
 DB 23 AGATTGCTCAGATTGGCGCT 3

RESULT 4  
 US-09-396-196G-104102/c  
 / Sequence 104102, Application US/09396196G  
 / Patent No. 6821724

GENERAL INFORMATION:  
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 104102

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-104102

Alignment Scores:  
 Pred. No.: 148 Length: 25  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-396-196G-104102 (1-25)

OY 18 ArgLeuLeuArgLeuGlyAla 24  
 DB 22 AGATTGCTCAGATTGGCGCT 2

RESULT 5

US-09-396-196G-104103/c

/ Sequence 104103, Application US/09396196G

/ Patent No. 6821724

GENERAL INFORMATION:  
 / APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 104103

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-104103

Alignment Scores:  
 Pred. No.: 148 Length: 25  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-396-196G-104103 (1-25)

US-10-048-046-2 (1-664) x US-09-396-1960-104103 (1-25)  
 QY 18 Argleuleuargyleuylala 24  
 |||||  
 DB 21 AGATTGCTCAATTGGGCGCT 1

RESULT 6  
 US-08-078-683A-35/c  
 / Sequence 35, Application US/08078683A  
 / Patent No. 5486599  
 / GENERAL INFORMATION:  
 / APPLICANT: Saunders, Scott  
 / APPLICANT: Bernfield, Merton  
 / APPLICANT: Kato, Masao  
 / TITLE OF INVENTION: Construction and Use of Synthetic  
 / TITLE OF INVENTION: Constructs Encoding Syndecan  
 / NUMBER OF SEQUENCES: 43  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSER: LAHIVE & COCKFIELD  
 / STREET: 60 State Street  
 / CITY: Boston  
 / STATE: MA  
 / COUNTRY: USA  
 / ZIP: 02109  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: ASCII (text)  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/078, 683A  
 / FILING DATE: 17-JUN-1993  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Vincent, Matthew P.  
 / REGISTRATION NUMBER: 36,709  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (617) 227-7400  
 / TELEFAX: (617) 227-5941  
 / INFORMATION FOR SEQ ID NO: 35:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 30 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: CDNA  
 / US-08-078-683A-35

Alignment Scores:  
 Pred. No.: 177 Length: 30  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-048-046-2 (1-664) x US-08-078-683A-35 (1-30)  
 QY 623 Sergluleuprovalalaval 629  
 |||||  
 DB 26 TCCGAGTTGCCGTTGCCAGTC 6

RESULT 7  
 US-08-471-970A-35/c  
 / Sequence 35, Application US/08471970A  
 / Patent No. 6531295  
 / GENERAL INFORMATION:  
 / APPLICANT: Saunders, Scott  
 / APPLICANT: Bernfield, Merton  
 / APPLICANT: Kato, Masao  
 / TITLE OF INVENTION: Construction and Use of Synthetic  
 / TITLE OF INVENTION: Constructs Encoding Syndecan

NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: LAHIVE & COCKFIELD  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII (text)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471, 970A  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/078, 683  
 FILING DATE: 17-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kara, Catherine J.  
 REGISTRATION NUMBER: P-41,106  
 REFERENCE/DOCKET NUMBER: CME-062DV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-471-970A-35

Alignment Scores:  
 Pred. No.: 177 Length: 30  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-08-471-970A-35 (1-30)  
 QY 623 Sergluleuprovalalaval 629  
 |||||  
 DB 26 TCCGAGTTGCCGTTGCCAGTC 6

RESULT 8  
 US-09-723-677B-35/c  
 / Sequence 35, Application US/09723677B  
 / Patent No. 6699968  
 / GENERAL INFORMATION:  
 / APPLICANT: SAUNDERS, SCOTT  
 / APPLICANT: BERNFIELD, MERTON  
 / APPLICANT: KATO, MASAO  
 / TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN  
 / FILE REFERENCE: 101353-151  
 / CURRENT APPLICATION NUMBER: US/09/723, 677B  
 / CURRENT FILING DATE: 2000-11-28  
 / PRIOR APPLICATION NUMBER: 08/471, 970  
 / PRIOR FILING DATE: 1995-06-06  
 / PRIOR APPLICATION NUMBER: 08/078, 683  
 / PRIOR FILING DATE: 1993-06-17  
 / PRIOR APPLICATION NUMBER: 07/856, 869  
 / PRIOR FILING DATE: 1992-03-24  
 / PRIOR APPLICATION NUMBER: 07/757, 654  
 / PRIOR FILING DATE: 1991-09-06  
 / PRIOR APPLICATION NUMBER: 07/746, 797  
 / PRIOR FILING DATE: 1991-08-12  
 / PRIOR APPLICATION NUMBER: 07/331, 585

PRIOR FILING DATE: 1989-03-29  
 NUMBER OF SEQ ID NOS: 46  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 35  
 LENGTH: 30  
 TYPE: DNA  
 ORGANISM: MUS BP  
 US-09-723-677B-35

## Alignment Scores:

Pred. No.:	177	Length:	30
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	3	Gaps:	0

US-10-048-046-2 (1-664) x US-09-723-677B-35 (1-30)

623 SerGiuleuProValAlaVal 629

DB 26 TCCGAGTCCGATTCCTCTCG 6

## RESULT 9

US-08-196-538-16  
 Sequence 16, Application US/08196538  
 Patent No. 5639608

GENERAL INFORMATION:  
 APPLICANT: Stanley Tabor  
 APPLICANT: Charles C. Richardson  
 TITLE OF INVENTION: USE OF SHORT OLIGONUCLEOTIDES AS PRIMERS  
 TITLE OF INVENTION: FOR DNA SEQUENCING  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 611 West Sixth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90017

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/196,538  
 FILING DATE: February 14, 1994  
 CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/985,468  
 FILING DATE: December 13, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 206/0930  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 33  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-196-538-16

## Alignment Scores:

Pred. No.:	193	Length:	33
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 1.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-048-046-2 (1-664) x US-08-196-538-16 (1-33)

623 ProArgValProPheSerSer 165

DB 6 CCGAGTCCGATTCCTCTCG 26

## RESULT 10

US-08-582-740-6  
 Sequence 6, Application US/08582740  
 Patent No. 6037324

GENERAL INFORMATION:  
 APPLICANT: Schwender, Charles F.  
 APPLICANT: Shroff, Hitesh N.  
 TITLE OF INVENTION: Inhibitors of MADCAM-1-Mediated  
 TITLE OF INVENTION: Interactions and Methods of Use Therefor  
 NUMBER OF SEQUENCES: 70  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Miltia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/582,740  
 FILING DATE: 04-JAN-1996  
 CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Brook, David B.  
 REGISTRATION NUMBER: 22,592  
 REFERENCE/DOCKET NUMBER: LKS95-12  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-9540  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 35 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

## Alignment Scores:

Pred. No.:	205	Length:	35
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	3	Gaps:	0

US-10-048-046-2 (1-664) x US-08-582-740-6 (1-35)

623 GlySerGlyGlyGlyIle 213

DB 7 GGATCCGATTCGAGGAGGAT 27

## RESULT 11

US-09-109-879-6  
 Sequence 6, Application US/09109879  
 Patent No. 6274556

GENERAL INFORMATION:  
 APPLICANT: Schwender, Charles F.  
 APPLICANT: Shroff, Hitesh N.  
 TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED  
 TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02421  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,879  
FILING DATE: 02-JUL-1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/00291  
FILING DATE: 03-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/582,740  
FILING DATE: 04-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS95-12A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 861-6240  
TELEFAX: (781) 861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-109-879-6

Alignment Scores:  
Pred. No.: 205 Length: 35  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.05% Indels: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-09-109-879-6 (1-35)

207 Glysarglyglyglyle 213  
DB 7. GGATCCGGTGGAGGAGGATT 27

RESULT 12  
US-08-582-740-63/C  
Sequence 63, Application US/08582740  
Patent No. 6037324  
GENERAL INFORMATION:  
APPLICANT: Schwender, Charles F.  
APPLICANT: Shroff, Hitesh N.  
TITLE OF INVENTION: Inhibitors of MADCAM-1-Mediated  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/582,740  
FILING DATE: 04-JAN-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS95-12  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 1..39  
US-08-582-740-63

Alignment Scores:  
Pred. No.: 227 Length: 39  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.05% Indels: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-08-582-740-63 (1-39)

207 Glysarglyglyglyle 213  
DB 24 GGATCCGGTGGAGGAGGATT 4

RESULT 13  
US-09-109-879-63/C  
Sequence 63, Application US/09109879  
Patent No. 6274556  
GENERAL INFORMATION:  
APPLICANT: Schwender, Charles F.  
APPLICANT: Shroff, Hitesh N.  
TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02421  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,879  
FILING DATE: 02-JUL-1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/00291  
FILING DATE: 03-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/582,740  
FILING DATE: 04-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS95-12A2

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781) 861-6240  
 TELEFAX: (781) 861-9540  
 INFORMATION FOR SEQ ID NO: 63:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 39 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..39  
 US-09-109-879-63

Alignment Scores:  
 Pred. No.: 227 Length: 39  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-109-879-63 (1-39)

OY 207 GlySerGlyGlyGlyIle 213  
 DB 24 GGATCCGCTGAGGAGCAATT 4

RESULT 14  
 US-07-931-473B-77/c  
 Sequence 77, Application US/07931473B  
 Patent No. 5270163  
 GENERAL INFORMATION:  
 APPLICANT: Larry Gold  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry J. Swanson  
 REGISTRATION NUMBER: 33,215  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 850-9900  
 TELEFAX: (303) 850-9401  
 INFORMATION FOR SEQ ID NO: 77:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 nucleotides  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-07-931-473B-77

Alignment Scores:  
 Pred. No.: 232 Length: 40  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-048-046-2 (1-664) x US-07-931-473B-77 (1-40)

OY 461 ProSerThrSerValSerLeu 467  
 DB 22 CCTTCGACATCCGTCGACTTG 2

RESULT 15  
 US-07-931-473B-109/c  
 Sequence 109, Application US/07931473B  
 Patent No. 5270163  
 GENERAL INFORMATION:  
 APPLICANT: Larry Gold  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry J. Swanson  
 REGISTRATION NUMBER: 33,215  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 850-9900  
 TELEFAX: (303) 850-9401  
 INFORMATION FOR SEQ ID NO: 109:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 nucleotides  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-07-931-473B-109

Alignment Scores:  
 Pred. No.: 232 Length: 40  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-048-046-2 (1-664) x US-07-931-473B-109 (1-40)

OY 461 ProSerThrSerValSerLeu 467  
 DB 22 CCTTCGACATCCGTCGACTTG 2

Search completed: January 12, 2006, 10:59:56  
 Job time : 317 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2006, 10:50:02 | Search time 1360 seconds

(with 403.402 Million cell updates/sec)

Title: US-10-048-046-2

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Sequence: 1 MERPEKQSPPOPMWRL.....VKAHAKFNHCQTRPKN 664

Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11076785

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Command line parameters:

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-DB=Published.Applications.NA.Main-QPWT-fastap-SUPFIX-01lg\_sz50.rnpsm  
-MINMATCH=0.1-LOOPEL=0-LOOPEXT=0-UNITS-bits-START=1-END=1-MATCH-01lg  
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-ALIGN=15-MODE=LOCAL-OUTPRMT=prc-NORM=ext-HEAPSIZ=500-MINLEN=50  
-USER=US10048046.ecgn\_1.1.1026-ecgnat\_10012006\_122940\_24178-NCPU=6-ICPU=3  
-DEV TIMEOUT=120-WARN TIMEOUT=30-THREADS=1-XGAPOP=60-XGAPEXT=60-FCGAPOP=6  
-FCGAPEXT=7-YGAPOP=60-YGAPEXT=60-DELOP=6-DELEXT=7

Database: Published.Applications.NA.Main:

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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.2	25	7	US-10-719-956-88030
2	8	1.2	25	10	US-11-036-317-24277
3	8	1.2	25	10	US-11-036-317-24394
4	8	1.2	25	10	US-11-036-317-60227
5	8	1.2	25	10	US-11-036-317-61246
6	8	1.2	25	10	US-11-036-317-67592
7	8	1.2	25	10	US-11-036-317-108822
8	8	1.2	25	10	US-11-036-317-131760

9	8	1.2	25	10	US-11-036-317-144618	Sequence 144618, A
10	8	1.2	25	10	US-11-036-317-153103	Sequence 153103, A
11	8	1.2	25	10	US-11-036-317-166836	Sequence 166836, A
12	8	1.2	25	10	US-11-036-317-198348	Sequence 198348, A
13	8	1.2	25	10	US-11-036-317-233307	Sequence 233307, A
14	8	1.2	25	10	US-11-036-317-259770	Sequence 259770, A
15	8	1.2	25	10	US-11-036-317-289125	Sequence 289125, A
16	8	1.2	25	10	US-11-036-317-320189	Sequence 320189, A
17	8	1.2	25	10	US-11-036-317-320979	Sequence 320979, A
18	8	1.2	25	10	US-11-036-317-364136	Sequence 364136, A
19	8	1.2	25	10	US-11-060-756-62495	Sequence 62495, A
20	8	1.2	25	10	US-11-060-756-62496	Sequence 62496, A
21	8	1.2	25	10	US-11-060-756-62497	Sequence 62497, A
22	8	1.2	25	10	US-11-060-756-62515	Sequence 62515, A
23	8	1.2	25	10	US-11-060-756-136129	Sequence 136129, A
24	8	1.2	25	10	US-11-060-756-152376	Sequence 152376, A
25	8	1.2	25	10	US-11-060-756-179266	Sequence 179266, A
26	8	1.2	25	10	US-11-060-756-184410	Sequence 184410, A
27	8	1.2	25	10	US-11-060-756-203366	Sequence 203366, A
28	8	1.2	25	10	US-11-060-756-203937	Sequence 203937, A
29	8	1.2	25	10	US-11-060-756-223559	Sequence 223559, A
30	8	1.2	25	10	US-11-060-756-236413	Sequence 236413, A
31	8	1.2	25	10	US-11-060-756-279102	Sequence 279102, A
32	8	1.2	25	10	US-11-060-756-283375	Sequence 283375, A
33	8	1.2	25	10	US-10-032-585-5047	Sequence 5047, A
34	7	1.1	22	6	US-10-098-263B-61049	Sequence 61049, A
35	7	1.1	25	5	US-10-098-263B-61050	Sequence 61050, A
36	7	1.1	25	5	US-10-098-263B-61677	Sequence 61677, A
37	7	1.1	25	7	US-10-681-773-66621	Sequence 66621, A
38	7	1.1	25	7	US-10-681-773-68399	Sequence 68399, A
39	7	1.1	25	7	US-10-719-956-1889	Sequence 1889, A
40	7	1.1	25	7	US-10-719-956-34455	Sequence 34455, A
41	7	1.1	25	7	US-10-719-956-114291	Sequence 114291, A
42	7	1.1	25	7	US-10-719-956-114292	Sequence 114292, A
43	7	1.1	25	7	US-10-719-956-328012	Sequence 328012, A
44	7	1.1	25	7	US-10-719-956-328012	Sequence 328012, A
45	7	1.1	25	7	US-10-719-956-328012	Sequence 328012, A

#### ALIGNMENTS

RESULT 1  
US-10-719-956-88030  
Sequence 88030, Application US/10719956  
Publication No. US20040146910A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
FILE REFERENCE: 3527.1  
CURRENT APPLICATION NUMBER: US/10/719,956  
PRIOR APPLICATION NUMBER: 2003-11-20  
PRIOR FILING DATE: 60/427,836  
NUMBER OF SEQ ID NOS: 699466  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 88030  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-10-719-956-88030

#### Alignment Scores:

Pred. No.: 72  
Score: 8.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 1.204  
DB: 7  
Length: 25  
Matches: 8  
Conservative: 0  
Mismatch: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-10-719-956-88030 (1-25)

303 ThrcvcllellecYsglnapleu 310

|||||



Db 1

ACCTGTATCATCTGTCAAGACTT 24

## RESULT 2

US-11-036-317-24277

Sequence 24277, Application US/11036317  
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 24277

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-24277

## Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)

Cy 48 SerPheProSerAnlyLeuVal 55

Db 1 TCTTCTTCCCGACATTAACGTC 24

## RESULT 3

US-11-036-317-24394

Sequence 24394, Application US/11036317  
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 24394

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-24394

## Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-24394 (1-25)

Cy 49 SerPheProSerAnlyLeuVal 56

Db 2 TCTTCTTCCCGACATTAACGTC 25

## RESULT 4

US-11-036-317-60227

Sequence 60227, Application US/11036317  
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 60227

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-60227

## Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)

Cy 49 SerPheProSerAnlyLeuVal 56

Db 1 TCTTCTTCCCGACATTAACGTC 24

## RESULT 5

US-11-036-317-61246

Sequence 61246, Application US/11036317  
Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 61246

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-61246

## Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)

Cy 47 AspleuSerPheProSerAnlyLeuVal 54

Db 2 GACCTCTTCTTCCCGACATTAAC 25

## RESULT 6

US-11-036-317-67592

Sequence 67592, Application US/11036317  
Publication No. US20050214823A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 67592
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-67592

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%  Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-67592 (1-25)

QY 46 CysAppLeuserPheProSerAen 53
DB 1 TGTGACCTCTCTTCCCGACGCAAT 24

RESULT 7
US-11-036-317-108822
/ Sequence 108822, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 108822
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-108822

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%  Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-108822 (1-25)

QY 388 AspMetLeuGlnProIlyValArg 395
DB 1 GATATGCTGCAACCCAAAGTCAGG 24

RESULT 8
US-11-036-317-131760
/ Sequence 131760, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 131760
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-131760

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%  Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-131760 (1-25)

QY 492 MetProAspArgArgAlaGluArg 499
DB 2 ATGCTGACCGAGAGCTGAACGG 25

RESULT 9
US-11-036-317-144618
/ Sequence 144618, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 144618
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-144618

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%  Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-144618 (1-25)

QY 413 AspValAspSerGluSerSerAsp 420
DB 2 GATGTCGACGAGTAATCTCAGAT 25

RESULT 10
US-11-036-317-153103
/ Sequence 153103, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317

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/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 131760
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-131760

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%  Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-131760 (1-25)

QY 492 MetProAspArgArgAlaGluArg 499
DB 2 ATGCTGACCGAGAGCTGAACGG 25

RESULT 9
US-11-036-317-144618
/ Sequence 144618, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 144618
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-144618

Alignment Scores:
Pred. No.: 72      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.20%  Indels: 0
DB: 10      Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-144618 (1-25)

QY 413 AspValAspSerGluSerSerAsp 420
DB 2 GATGTCGACGAGTAATCTCAGAT 25

RESULT 10
US-11-036-317-153103
/ Sequence 153103, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317

```

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CURRENT FILING DATE: 2005-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
PRIORITY FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 153103
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-048-046-2 (1-664) x US-11-036-317-153103 (1-25)

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
DB: 10
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-153103 (1-25)

QY 405 ArgArgArgGlyCysAspLeuSer 412
DB 2 TCAGAGGAGCTGCTGAGACTGCTCT 25

RESULT 11
US-11-036-317-166836
Sequence 166836, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIORITY FILING DATE: 2004-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 166836
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-166836

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
DB: 10
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-166836 (1-25)

QY 42 ArgArgArgGlyCysAspLeuSer 49
DB 2 AGGAGAGAGGCTGCTGAGACTGCTCT 25

RESULT 12
US-11-036-317-198348
Sequence 198348, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIORITY FILING DATE: 2004-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
SEQ ID NO: 153103
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-153103

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```

NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 198348
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-198348

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
DB: 10
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-198348 (1-25)

QY 42 ArgArgArgGlyCysAspLeuSer 49
DB 1 AGGAGAGAGGCTGCTGAGACTGCTCT 24

RESULT 13
US-11-036-317-233307
Sequence 233307, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIORITY FILING DATE: 2004-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 233307
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-233307

Alignment Scores:
Pred. No.: 72
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.20%
DB: 10
Length: 25
Matches: 8
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-233307 (1-25)

QY 559 IleLeuIysAsnTyrLeuAlaThr 566
DB 2 ATCTGAAGATTAATCTGCAACC 25

RESULT 14
US-11-036-317-259770
Sequence 259770, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIORITY FILING DATE: 2004-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 259770

```

/ LENGTH: 25  
 / TYPE: DNA  
 / ORGANISM: Mus musculus  
 US-11-036-317-259770

## Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-259770 (1-25)

OY 41 G1YATGATGATGGLYCYGAAPLEU 48  
 |||||  
 DB 2 GGAAAGAGAGAGGCTGTGACCTC 25

## RESULT 15

US-11-036-317-289125  
 / Sequence 289125, Application US/11036317  
 / Publication No. US20050214823A1  
 / GENERAL INFORMATION:

/ APPLICANT: Blume, John  
 / TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
 / FILE REFERENCE: 3654.1  
 / CURRENT APPLICATION NUMBER: US/11/036,317  
 / CURRENT FILING DATE: 2005-01-13  
 / PRIOR APPLICATION NUMBER: US 60/536,639  
 / PRIOR FILING DATE: 2004-01-13  
 / NUMBER OF SEQ ID NOS: 991174  
 / SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 / SEQ ID NO 289125

/ LENGTH: 25  
 / TYPE: DNA  
 / ORGANISM: Mus musculus  
 US-11-036-317-289125

## Alignment Scores:

Pred. No.:	72	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	10	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-289125 (1-25)

OY 558 AP1LEULEUYEAENTYFLEUALA 565  
 |||||  
 DB 1 GACATCCTGAAGAAATTACCTGACA 24

Search completed: January 12, 2006, 13:54:49  
 Job time : 1361 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2006, 10:56:48 | Search time 294 Seconds  
(without alignments)  
1827.916 Million cell updates/sec

Title: US-10-048-046-2  
Perfect score: 664  
Sequence: 1 MERPEKQSPPPQWRLT.....VAAHAKMKNHCEQTRFKN 664

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Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 6038314 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 11530093

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=50  
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-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Published Applications NA New.\*

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5: /csn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
6: /csn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
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8: /csn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
9: /csn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
10: /csn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	7	1.1	21	6	US-10-310-914A-42895
2	7	1.1	21	6	US-10-310-914A-638790
3	7	1.1	21	6	US-10-310-914A-814305
4	7	1.1	21	6	US-10-310-914A-1320691
5	7	1.1	22	6	US-10-310-914A-56004
6	7	1.1	22	6	US-10-310-914A-374833
7	7	1.1	22	6	US-10-310-914A-626661
8	7	1.1	22	6	US-10-310-914A-1064918

9	7	1.1	22	6	US-10-310-914A-1205143	Sequence 1205143, A
10	7	1.1	23	6	US-10-310-914A-42890	Sequence 42890, A
11	7	1.1	23	6	US-10-310-914A-374831	Sequence 374831, A
12	7	1.1	23	6	US-10-310-914A-482394	Sequence 482394, A
13	7	1.1	23	6	US-10-310-914A-542344	Sequence 542344, A
14	7	1.1	23	6	US-10-310-914A-815510	Sequence 815510, A
15	7	1.1	23	6	US-10-310-914A-1320692	Sequence 1320692, A
16	7	1.1	23	6	US-10-310-914A-1363456	Sequence 1363456, A
17	7	1.1	24	6	US-10-310-914A-838918	Sequence 838918, A
18	7	1.1	24	6	US-10-310-914A-1060225	Sequence 1060225, A
19	7	1.1	24	6	US-10-310-914A-1128181	Sequence 1128181, A
20	7	1.1	24	6	US-10-310-914A-1267239	Sequence 1267239, A
21	7	1.1	24	6	US-10-310-914A-1363461	Sequence 1363461, A
22	7	1.1	25	6	US-10-310-914A-97707	Sequence 97707, A
23	7	1.1	25	6	US-10-310-914A-222932	Sequence 222932, A
24	7	1.1	25	6	US-10-310-914A-57609	Sequence 57609, A
25	7	1.1	25	6	US-10-310-914A-1363459	Sequence 1363459, A
26	7	1.1	25	6	US-11-121-849-239450	Sequence 239450, A
27	7	1.1	25	7	US-11-121-849-331027	Sequence 331027, A
28	7	1.1	25	7	US-11-121-849-331028	Sequence 331028, A
29	7	1.1	25	7	US-11-121-849-331029	Sequence 331029, A
30	7	1.1	25	7	US-11-121-849-415066	Sequence 415066, A
31	7	1.1	25	7	US-11-121-849-428097	Sequence 428097, A
32	7	1.1	25	7	US-11-121-849-428097	Sequence 428097, A
33	7	1.1	25	7	US-11-121-849-428098	Sequence 428098, A
34	7	1.1	25	7	US-11-121-849-568626	Sequence 568626, A
35	7	1.1	26	6	US-10-310-914A-1004305	Sequence 1004305, A
36	7	1.1	27	6	US-10-310-914A-815792	Sequence 815792, A
37	7	1.1	27	6	US-10-310-914A-1004294	Sequence 1004294, A
38	7	1.1	32	6	US-10-939-294A-16935	Sequence 16935, A
39	7	1.1	32	6	US-10-939-294A-17619	Sequence 17619, A
40	7	1.1	32	6	US-10-939-294A-19354	Sequence 19354, A
41	7	1.1	32	6	US-10-939-294A-17818	Sequence 17818, A
42	7	1.1	18	6	US-10-310-914A-89188	Sequence 89188, A
43	6	0.9	18	6	US-10-310-914A-144700	Sequence 144700, A
44	6	0.9	18	6	US-10-310-914A-144700	Sequence 144700, A
45	6	0.9	18	6	US-10-310-914A-176873	Sequence 176873, A

#### ALIGNMENTS

RESULT 1  
US-10-310-914A-42895  
Sequence 42895, Application US/10310914A  
Publication No. US2006000322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087, 0200, CPUS01  
CURRENT APPLICATION NUMBER: US/10/310, 914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 42895  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-42895

#### Alignment Scores:

Pred. No.: 380  
Score: 7.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 1.05%  
Length: 21  
Matches: 7  
Conservative: 0  
Mismatch: 0  
Indel: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-42895 (1-21)

150 GYALAGYALAGYATGAGY 156

|||||

CRP of 6/29/3 338  
11/14/02

Db 1 GGGGCGGCGCGGCGGCGG 21

## RESULT 2

US-10-310-914A-638790/C  
Sequence 638790, Application US/10310914A  
Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kyuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 638790

LENGTH: 21

TYPE: RNA

ORGANISM: Human

US-10-310-914A-638790

Alignment Scores:

Pred. No.: 380

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.05%

DB: 6

Length: 21

Matches: 7

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-638790 (1-21)

Db 21

RESULT 3

US-10-310-914A-814306

Sequence 814306, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kyuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 814306

LENGTH: 21

TYPE: RNA

ORGANISM: Human

US-10-310-914A-814306

Alignment Scores:

Pred. No.: 380

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.05%

DB: 6

Length: 21

Matches: 7

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-814306 (1-21)

Db 150

RESULT 4

US-10-310-914A-1320691/C

Sequence 1320691, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kyuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1320691

LENGTH: 21

TYPE: RNA

ORGANISM: Human

US-10-310-914A-1320691

Alignment Scores:

Pred. No.: 380

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.05%

DB: 6

Length: 21

Matches: 7

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-1320691 (1-21)

Db 21

RESULT 5

US-10-310-914A-56004/C

Sequence 56004, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kyuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 56004

LENGTH: 22

TYPE: RNA

ORGANISM: Human

US-10-310-914A-56004

Alignment Scores:

Pred. No.: 397

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.05%

DB: 6

Length: 22

Matches: 7

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-56004 (1-22)

Db 495

RESULT 6

US-10-310-914A-374833

Sequence 374833, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kyuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 374833

LENGTH: 21

TYPE: RNA

ORGANISM: Human

US-10-310-914A-374833

Alignment Scores:

Pred. No.: 380

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.05%

DB: 6

Length: 21

Matches: 7

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-374833 (1-21)

Db 21

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/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 374833
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-374833

Alignment Scores:
Pred. No.: 397          Length: 22
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.05%      Indels: 0
DB: 6                  Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-374833 (1-22)

Qy 150 G1YAlAG1YAlAG1YArgG1Y 156
Db 2 GGGGCGAGCGCGCGCGCGCGG 22

RESULT 7
US-10-310-914A-626661
/ Sequence 626661, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 626661
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-626661

Alignment Scores:
Pred. No.: 397          Length: 22
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.05%      Indels: 0
DB: 6                  Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-626661 (1-22)

Qy 150 G1YAlAG1YAlAG1YArgG1Y 156
Db 2 GGGGCGAGCGCGCGCGCGG 22

RESULT 8
US-10-310-914A-1064918/c
/ Sequence 1064918, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
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/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1064918
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1064918

Alignment Scores:
Pred. No.: 397          Length: 22
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.05%      Indels: 0
DB: 6                  Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-1064918 (1-22)

Qy 160 ArgValProPseSerSerPro 166
Db 22 AGGTCACACGCTCTCCCA 2

RESULT 9
US-10-310-914A-1205143/c
/ Sequence 1205143, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1205143
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1205143

Alignment Scores:
Pred. No.: 397          Length: 22
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 1.05%      Indels: 0
DB: 6                  Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-1205143 (1-22)

Qy 156 G1YAlAaPProArGValPro 162
Db 21 GGAGCGAGCCCTAGGTCGCC 1

RESULT 10
US-10-310-914A-42890
/ Sequence 42890, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310.914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 42890
/ LENGTH: 23
/ TYPE: RNA
/ ORGANISM: Human
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US-10-310-914A-42890

Alignment Scores:

Pred. No.: 414 Length: 23  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-42890 (1-23)

QY 150 G1YALAG1YALAG1YARG1Y 156  
 DB 3 GGGCGGGCGGGCGGGCGGGCGG 23

RESULT 11  
 US-10-310-914A-374831  
 Sequence 374831, Application US/10310914A  
 Publication No. US20060003322A1  
 GENERAL INFORMATION:  
 APPLICANT: Bentwich, Isaac  
 APPLICANT: Shlier, Kiyazet  
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 FILE REFERENCE: 06087.0200.CPUS01  
 CURRENT APPLICATION NUMBER: US/10/310,914A  
 CURRENT FILING DATE: 2002-12-06  
 NUMBER OF SEQ ID NOS: 1388402  
 SOFTWARE: Patent in version 3.3  
 SEQ ID NO 374831  
 LENGTH: 23  
 TYPE: RNA  
 ORGANISM: Human  
 US-10-310-914A-374831

Alignment Scores:

Pred. No.: 414 Length: 23  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-374831 (1-23)

QY 150 G1YALAG1YALAG1YARG1Y 156  
 DB 1 GGGCGGGCGGGCGGGCGGGCGG 21

RESULT 12

US-10-310-914A-482394  
 Sequence 482394, Application US/10310914A  
 Publication No. US20060003322A1  
 GENERAL INFORMATION:  
 APPLICANT: Bentwich, Isaac  
 APPLICANT: Shlier, Kiyazet  
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 FILE REFERENCE: 06087.0200.CPUS01  
 CURRENT APPLICATION NUMBER: US/10/310,914A  
 CURRENT FILING DATE: 2002-12-06  
 NUMBER OF SEQ ID NOS: 1388402  
 SOFTWARE: Patent in version 3.3  
 SEQ ID NO 482394  
 LENGTH: 23  
 TYPE: RNA  
 ORGANISM: Human  
 US-10-310-914A-482394

Alignment Scores:

Pred. No.: 414 Length: 23  
 Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-482394 (1-23)

QY 18 ArgLeuLeuArgLeuG1YAla 24  
 DB 3 AGGCUUCUACGCCUUGGGGCU 23

RESULT 13

US-10-310-914A-542344/c  
 Sequence 542344, Application US/10310914A  
 Publication No. US20060003322A1  
 GENERAL INFORMATION:  
 APPLICANT: Bentwich, Isaac  
 APPLICANT: Shlier, Kiyazet  
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 FILE REFERENCE: 06087.0200.CPUS01  
 CURRENT APPLICATION NUMBER: US/10/310,914A  
 CURRENT FILING DATE: 2002-12-06  
 NUMBER OF SEQ ID NOS: 1388402  
 SOFTWARE: Patent in version 3.3  
 SEQ ID NO 542344  
 LENGTH: 23  
 TYPE: RNA  
 ORGANISM: Human  
 US-10-310-914A-542344

Alignment Scores:

Pred. No.: 414 Length: 23  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-542344 (1-23)

QY 184 LeuPheProThrAlaSerAla 190  
 DB 23 CTGTTCCCAAGCCAGCGCC 3

RESULT 14

US-10-310-914A-815510/c  
 Sequence 815510, Application US/10310914A  
 Publication No. US20060003322A1  
 GENERAL INFORMATION:  
 APPLICANT: Bentwich, Isaac  
 APPLICANT: Shlier, Kiyazet  
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 FILE REFERENCE: 06087.0200.CPUS01  
 CURRENT APPLICATION NUMBER: US/10/310,914A  
 CURRENT FILING DATE: 2002-12-06  
 NUMBER OF SEQ ID NOS: 1388402  
 SOFTWARE: Patent in version 3.3  
 SEQ ID NO 815510  
 LENGTH: 23  
 TYPE: RNA  
 ORGANISM: Human  
 US-10-310-914A-815510

Alignment Scores:

Pred. No.: 414 Length: 23  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.05% Indels: 0  
 DB: 6 Gaps: 0



US-10-048-046-2 (1-664) x US-10-310-914A-815510 (1-23)

Qy 150 GYALAGLYALAGLYARGG1Y 156  
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 Db 21 GGTGCGAGAGCTGCGCGAGGT 1

RESULT 15

US-10-310-914A-1320692/c  
 / Sequence 1320692, Application US/10310914A  
 / Publication No. US20060003322A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Benwich, Isaac  
 / APPLICANT: Shiler, Kuzat  
 / TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 / TITLE OF INVENTION: uses thereof  
 / FILE REFERENCE: 06087,0200,CPUS01  
 / CURRENT APPLICATION NUMBER: US/10/310,914A  
 / NUMBER OF SEQ ID NOS: 138402  
 / SOFTWARE: Patent version 3.3  
 / SEQ ID NO 1320692  
 / LENGTH: 23  
 / TYPE: RNA  
 / ORGANISM: Human  
 US-10-310-914A-1320692

Alignment Scores:

Pred. No.:	414	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.05%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-310-914A-1320692 (1-23)

Qy 20 LeuARGLeuGLYALAGLU 26  
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 Db 23 CTAAGCTTGGGCGCGAGGAG 3

Search completed: January 12, 2006, 13:59:49  
 Job time : 295 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2006, 10:25:28 / Search time 8980 Seconds

(without alignments)  
4088.375 Million cell updates/sec

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Perfect score: 664  
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Searched: 73147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 87479736

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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-TRANS=human40.cdd -LIST=45 -DOCALLIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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2	8	1.2	25	US-09-954-4278-238351	Sequence 238351, A
3	8	1.2	25	US-09-954-4278-238353	Sequence 238353, A
4	8	1.2	25	US-09-954-4278-238358	Sequence 238358, A
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38     1.2      25 66 US-11-060-756-225655      Sequence 225655, A
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45     1.2      25 81 US-60-545-213-62496      Sequence 62496, A

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## ALIGNMENTS

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RESULT 1
US-09-953-570A-36815/c
; Sequence 36815, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/332,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 36815
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-36815

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Query Match: 1.20%      Indels: 0
DB: 37      Gaps: 0

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US-10-048-046-2 (1-664) x US-09-953-570A-36815 (1-25)
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DB 24 ACCTTACCAAGTGGCACCGTGAAT 1

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RESULT 2
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; Sequence 238351, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 238351
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-238351

Alignment Scores:
Pred. No.: 716      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 37      Gaps: 0

```

```

US-10-048-046-2 (1-664) x US-09-954-427A-238351 (1-25)
QY 304 Cytellelecyglnapleu 311
DB 2 TGATCATCTGTCAAGACTTCTG 25

RESULT 3
US-09-954-427A-238353
; Sequence 238353, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 238353
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-238353

```

```

Alignment Scores:
Pred. No.: 716      Length: 25
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 1.20%      Indels: 0
DB: 37      Gaps: 0

```

```
US-10-048-046-2 (1-664) x US-09-954-427A-238353 (1-25)
```

```

QY 302 LeuthrCyelleleCyeglnasp 309
DB 2 CTAACTTATCATCTGTCAAGAC 25

```

```

RESULT 4
US-09-954-427A-238358
; Sequence 238358, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome

```

```
/ FILE REFERENCE: 3112.1
/ CURRENT APPLICATION NUMBER: US/09/954,427A
/ PRIOR FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/233,166
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 420907
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 238358
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus Norvegicus
/ US-09-954-427A-238358

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 37 Gaps: 0

US-10-048-046-2 (1-664) x US-09-954-427A-238358 (1-25)

QY 300 GlnThrLeuThrCysAlaIleCys 307
DB 2 GAGACACTAACCGTATCATCTCT 25

RESULT 5
US-09-954-427A-238359
/ Sequence 238359, Application US/09954427A
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
/ FILE REFERENCE: 3112.1
/ CURRENT APPLICATION NUMBER: US/09/954,427A
/ PRIOR FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/233,166
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 420907
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 238359
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus Norvegicus
/ US-09-954-427A-238359

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 37 Gaps: 0

US-10-048-046-2 (1-664) x US-09-954-427A-238359 (1-25)

QY 294 LysProAlaPlyMetGluGluThr 301
DB 2 AAACACGACAGATGAGAGAGACA 25

RESULT 6
US-09-956-604-29770/C
/ Sequence 29770, Application US/09956604
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Becherichia coli
/ FILE REFERENCE: 3117.1
/ CURRENT APPLICATION NUMBER: US/09/956,604
/ PRIOR FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/234,049
/ PRIOR FILING DATE: 2000-09-19
/ NUMBER OF SEQ ID NOS: 141629
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604B-29770

Alignment Scores:
```

```
/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604-29770

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604-29770 (1-25)

QY 462 SerThrSerValSerLeuThrThr 469
DB 25 AGTACGTCGATCGTACTACTACA 2

RESULT 7
US-09-956-604A-29770/C
/ Sequence 29770, Application US/09956604A
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Becherichia coli
/ FILE REFERENCE: 3117.1
/ CURRENT APPLICATION NUMBER: US/09/956,604A
/ PRIOR FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/234,049
/ PRIOR FILING DATE: 2000-09-19
/ NUMBER OF SEQ ID NOS: 141629
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604A-29770

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604A-29770 (1-25)

QY 462 SerThrSerValSerLeuThrThr 469
DB 25 AGTACGTCGATCGTACTACTACA 2

RESULT 8
US-09-956-604B-29770/C
/ Sequence 29770, Application US/09956604B
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Becherichia coli
/ FILE REFERENCE: 3117.1
/ CURRENT APPLICATION NUMBER: US/09/956,604B
/ PRIOR FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/234,049
/ PRIOR FILING DATE: 2000-09-19
/ NUMBER OF SEQ ID NOS: 141629
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 29770
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Becherichia coli
/ US-09-956-604B-29770

Alignment Scores:
```

Pred. No.: 716 Length: 25  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.20% Indels: 0  
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604B-29770 (1-25)

OY 462 SerTherSevalSerleuthrthr 469  
DB 25 AGRACGTCGATCGCTACCTACA 2

RESULT 9  
US-10-719-956-88030  
Sequence 88030, Application US/10719956  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
FILE REFERENCE: 3527.1  
CURRENT APPLICATION NUMBER: US/10/719,956  
PRIOR FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,836  
NUMBER OF SEQ ID NOS: 699466  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 88030  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-10-719-956-88030

Alignment Scores:  
Pred. No.: 716 Length: 25  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.20% Indels: 0  
DB: 61 Gaps: 0

US-10-048-046-2 (1-664) x US-10-719-956-88030 (1-25)

OY 303 ThrCyjleleleCy3glnaapleu 310  
DB 1 ACCTGATCATCTGCTCAACCTT 24

RESULT 10  
US-11-036-317-24277  
Sequence 24277, Application US/11036317  
GENERAL INFORMATION:  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
PRIOR FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 24277  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-24277

Alignment Scores:  
Pred. No.: 716 Length: 25  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.20% Indels: 0  
DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)  
OY 48 LeuSerPheProSerAenlyLeuVal 55  
DB 1 CTCCTTCCCGACCATTAACCTG 24

RESULT 11  
US-11-036-317-24394  
Sequence 24394, Application US/11036317  
GENERAL INFORMATION:  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
PRIOR FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 24394  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-24394

Alignment Scores:  
Pred. No.: 716 Length: 25  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.20% Indels: 0  
DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-24394 (1-25)

OY 49 SerPheProSerAenlyLeuVal 56  
DB 2 TCTTCCCGACCATTAACCTGTC 25

RESULT 12  
US-11-036-317-60227  
Sequence 60227, Application US/11036317  
GENERAL INFORMATION:  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
PRIOR FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 60227  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-60227

Alignment Scores:  
Pred. No.: 716 Length: 25  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.20% Indels: 0  
DB: 66 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)

OY 49 SerPheProSerAenlyLeuVal 56  
DB 1 TCTTCCCGACCATTAACCTGTC 25

Db 1 TCTTCCCGACATTAAGTGTG 24

RESULT 13

US-11-036-317-61246

/ Sequence 61246, Application US/11036317

/ GENERAL INFORMATION:

/ APPLICANT: Williams, Alan

/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

/ FILE REFERENCE: 3654.1

/ CURRENT APPLICATION NUMBER: US/11/036,317

/ PRIOR FILING DATE: 2005-01-13

/ PRIOR APPLICATION NUMBER: US 60/536,639

/ NUMBER OF SEQ ID NOS: 991174

/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

/ SEQ ID NO 61246

/ LENGTH: 25

/ TYPE: DNA

/ ORGANISM: Mus musculus

US-11-036-317-61246

Alignment Scores:

Pred. No.:	716	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	66	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)

CY 47 AppLeuserPhroSerghenly 54

DB 2 GACCTCTCTTCCCGACATTA 25

RESULT 14

US-11-036-317-67592

/ Sequence 67592, Application US/11036317

/ GENERAL INFORMATION:

/ APPLICANT: Williams, Alan

/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

/ FILE REFERENCE: 3654.1

/ CURRENT APPLICATION NUMBER: US/11/036,317

/ PRIOR FILING DATE: 2005-01-13

/ PRIOR APPLICATION NUMBER: US 60/536,639

/ NUMBER OF SEQ ID NOS: 991174

/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

/ SEQ ID NO 67592

/ LENGTH: 25

/ TYPE: DNA

/ ORGANISM: Mus musculus

US-11-036-317-67592

Alignment Scores:

Pred. No.:	716	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	66	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-67592 (1-25)

CY 46 CyapLeuserPhroSerghen 53

DB 1 TGTGACCTCTTCCCGACAT 24

RESULT 15

US-11-036-317-108822

/ Sequence 108822, Application US/11036317

/ GENERAL INFORMATION:

/ APPLICANT: Williams, Alan

/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

/ FILE REFERENCE: 3654.1

/ CURRENT APPLICATION NUMBER: US/11/036,317

/ PRIOR FILING DATE: 2005-01-13

/ PRIOR APPLICATION NUMBER: US 60/536,639

/ NUMBER OF SEQ ID NOS: 991174

/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

/ SEQ ID NO 108822

/ LENGTH: 25

/ TYPE: DNA

/ ORGANISM: Mus musculus

US-11-036-317-108822

Alignment Scores:

Pred. No.:	716	Length:	25
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.20%	Indels:	0
DB:	66	Gaps:	0

US-10-048-046-2 (1-664) x US-11-036-317-108822 (1-25)

CY 388 AppMetLeugInProlyseValnrg 395

DB 1 GATATGCTGCAACCAAGTCAGG 24

Search completed: January 12, 2006, 13:29:43

Job time : 8982 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2006, 10:27:18 / Search time 130 seconds  
(without alignments)  
2639.356 Million cell updates/sec

Title: US-10-048-046-2  
Perfect score: 664  
Sequence: 1 MERPEKQSPPPQPMGRLL.....VAAHAKMKNICGQTRPRN 664

Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1087749 seqs, 258370665 residues

Total number of hits satisfying chosen parameters: 208730

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n\_model -DEV=xlh  
-Q=/cgn2\_1/USPRO\_SPEC/US10048046/Runat\_10012006\_122940\_24163/app\_query.fasta.1.839  
-DB=Pending\_Patents\_NA\_New -OPMT=fastcap -SUFFIX=01lg\_gz50.tmpn -MINMATCH=0.1  
-LOOCL=0 -LOOEXT=0 -UNIT8=bits -START=1 -END=1 -MATRIX=01lg  
-TRANS=numat40.cdi -LIST=45 -DOCLIGN=200 -HBR SCORE=quality -THR\_MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTPR=prco -NORM=ext -HBRPRTS=500 -MINLEN=0 -MAXLEN=50  
-USER=US10048046@cgn2\_1.1.78 @runat\_10012006\_122940\_24163 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPLLOCK=100 -LONGLOC  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/pdata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/pdata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/pdata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/pdata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/pdata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/pdata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/pdata/1/pna/US11\_NEW\_COMB.seq.\*  
8: /cgn2\_6/pdata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	6	0.9	19	US-10-562-561-562	Sequence 562, App
C 2	6	0.9	19	US-10-562-561-562	Sequence 887, App
C 3	6	0.9	20	US-10-527-552-18	Sequence 18, App
C 4	6	0.9	20	US-11-294-621-70	Sequence 70, App
C 5	6	0.9	20	US-11-317-798-5513	Sequence 5513, App
C 6	6	0.9	21	US-60-742-219-4800	Sequence 4800, App
C 7	6	0.9	22	US-11-130-645B-8449	Sequence 8449, App
C 8	6	0.9	22	US-11-130-645B-10537	Sequence 10537, App
C 9	6	0.9	22	US-11-130-645B-10712	Sequence 10712, App
C 10	6	0.9	22	US-11-130-645B-13922	Sequence 13922, App

11	6	0.9	22	7	US-11-130-645B-13924	Sequence 13924, App
12	6	0.9	22	7	US-11-130-645B-13925	Sequence 13925, App
13	6	0.9	22	7	US-11-130-645B-16045	Sequence 16045, App
14	6	0.9	23	6	US-10-515-051-78	Sequence 78, App
15	6	0.9	25	7	US-11-067-260-59	Sequence 59, App
16	6	0.9	25	7	US-11-067-260-61	Sequence 61, App
17	6	0.9	25	7	US-11-067-260-65	Sequence 65, App
18	6	0.9	25	7	US-11-067-260-67	Sequence 67, App
19	6	0.9	25	7	US-11-067-260-92	Sequence 92, App
C 20	6	0.9	25	7	US-11-315-777-1	Sequence 1, App
C 21	6	0.9	25	7	US-11-319-873-1	Sequence 1, App
C 22	6	0.9	25	8	US-60-735-352-12	Sequence 12, App
C 23	6	0.9	26	6	US-10-149-553B-17	Sequence 37, App
C 24	6	0.9	27	7	US-11-301-360-1077	Sequence 1077, App
C 25	6	0.9	29	7	US-11-317-798-5547	Sequence 5547, App
C 26	6	0.9	30	1	PCT-US05-10912-2441	Sequence 2441, App
C 27	6	0.9	30	8	US-60-751-196-10	Sequence 10, App
C 28	6	0.9	30	8	US-60-751-196-15	Sequence 15, App
C 29	6	0.9	31	7	US-11-262-284-10	Sequence 10, App
C 30	6	0.9	33	7	US-11-275-346-2	Sequence 2, App
C 31	6	0.9	34	7	US-11-067-260-75	Sequence 75, App
C 32	6	0.9	34	7	US-11-317-798-3675	Sequence 3675, App
C 33	6	0.9	35	5	US-09-142-471D-12	Sequence 12, App
C 34	6	0.9	35	5	US-09-142-471D-13	Sequence 13, App
C 35	6	0.9	35	7	US-11-067-260-111	Sequence 111, App
C 36	6	0.9	35	7	US-11-067-260-5302	Sequence 5302, App
C 37	6	0.9	38	7	US-11-067-260-106	Sequence 106, App
C 38	6	0.9	39	7	US-11-067-260-73	Sequence 73, App
C 39	6	0.9	41	7	US-11-067-260-63	Sequence 63, App
C 40	6	0.9	41	7	US-11-067-260-69	Sequence 69, App
C 41	6	0.9	41	7	US-11-067-260-77	Sequence 77, App
C 42	6	0.9	41	7	US-11-067-260-87	Sequence 87, App
C 43	6	0.9	42	6	US-10-199-820A-102	Sequence 102, App
C 44	6	0.9	42	7	US-11-067-260-71	Sequence 71, App
C 45	6	0.9	42	7	US-11-067-260-94	Sequence 94, App

## ALIGNMENTS

RESULT 1  
US-10-562-561-562/c  
Sequence 562, Application US/10562561  
GENERAL INFORMATION:  
APPLICANT: Sirta Therapeutics, Inc.  
APPLICANT: McSwigen, James  
TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using  
FILE REFERENCE: 400/166 (MBH02-728-G)  
CURRENT APPLICATION NUMBER: US/10/562, 561  
PRIOR FILING DATE: 2005-12-28  
PRIOR APPLICATION NUMBER: US 10/607933  
PRIOR FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US 09/930423  
PRIOR FILING DATE: 2001-08-15  
PRIOR APPLICATION NUMBER: PCT/US03/04710  
PRIOR FILING DATE: 2003-02-18  
PRIOR APPLICATION NUMBER: US 10/205309  
PRIOR FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: PCT/US04/16390  
PRIOR FILING DATE: 2004-05-24  
PRIOR APPLICATION NUMBER: US 10/826966  
PRIOR FILING DATE: 2004-04-16  
PRIOR APPLICATION NUMBER: US 10/757803  
PRIOR FILING DATE: 2004-01-14  
PRIOR APPLICATION NUMBER: US 10/720448  
PRIOR FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: US 10/693059  
PRIOR FILING DATE: 2003-10-23  
PRIOR APPLICATION NUMBER: US 10/444853  
PRIOR FILING DATE: 2003-05-23  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1904

SOFTWARE: Patentin version 3.3  
SEQ ID NO 562  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sRNA sense  
US-10-562-561-562

Alignment Scores:  
Pred. No.: 885 Length: 19  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.90% Indels: 0  
Gaps: 0  
DB: 6

US-10-048-046-2 (1-664) x US-10-562-561-562 (1-19)

QY 193 ThrgUpProSerProAla 198  
DB 19 ACAGAGCCAGCCCTGCT 2

RESULT 2  
US-10-562-561-887  
Sequence 887, Application US/10562561  
GENERAL INFORMATION:  
APPLICANT: Sitma Therapeutics, Inc.  
APPLICANT: McSwiggen, James  
APPLICANT: Belgelman, Leonid  
TITLE OF INVENTION: RNA interference Mediated Treatment of Alzheimer's Disease Using  
TITLE OF INVENTION: Short interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/166 (MAH802-728-G)  
CURRENT APPLICATION NUMBER: US/10/562,561  
PRIOR FILING DATE: 2005-12-28  
PRIOR APPLICATION NUMBER: US 10/607933  
PRIOR FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US 09/930423  
PRIOR FILING DATE: 2001-08-15  
PRIOR APPLICATION NUMBER: PCT/US03/04710  
PRIOR FILING DATE: 2003-02-18  
PRIOR APPLICATION NUMBER: US 10/205309  
PRIOR FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: PCT/US04/16390  
PRIOR FILING DATE: 2004-05-24  
PRIOR APPLICATION NUMBER: US 10/826966  
PRIOR FILING DATE: 2004-04-16  
PRIOR APPLICATION NUMBER: US 10/757803  
PRIOR FILING DATE: 2004-01-14  
PRIOR APPLICATION NUMBER: US 10/720448  
PRIOR FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: US 10/693059  
PRIOR FILING DATE: 2003-10-23  
PRIOR APPLICATION NUMBER: US 10/444853  
PRIOR FILING DATE: 2003-05-23  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1904  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 887  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-562-561-887

Alignment Scores:  
Pred. No.: 885 Length: 19  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.90% Indels: 0  
Gaps: 0  
DB: 6

US-10-048-046-2 (1-664) x US-10-562-561-887 (1-19)

QY 193 ThrgUpProSerProAla 198  
DB 1 ACAGAGCCAGCCCTGCT 18

RESULT 3  
US-10-527-552-18  
Sequence 18, Application US/10527552  
GENERAL INFORMATION:  
APPLICANT: Sandoz GmbH  
TITLE OF INVENTION: Process for production of cephalosporin C  
FILE REFERENCE: 1B/G-32677A/BCK  
CURRENT APPLICATION NUMBER: US/10/527,552  
CURRENT FILING DATE: 2005-03-11  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 18  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-10-527-552-18

Alignment Scores:  
Pred. No.: 926 Length: 20  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.90% Indels: 0  
Gaps: 0  
DB: 6

US-10-048-046-2 (1-664) x US-10-527-552-18 (1-20)

QY 208 SerGlyGlyGlyGly 213  
DB 1 TCGGAGGTGGAGGATT 18

RESULT 4  
US-11-294-621-70/C  
Sequence 70, Application US/11294621  
GENERAL INFORMATION:  
APPLICANT: BELL, DAPHNE WINIFRED  
APPLICANT: HABER, DANIEL A.  
APPLICANT: JARNE, PAST ANTERO  
APPLICANT: JOHNSON, BRUCE E.  
APPLICANT: LYNCH, THOMAS J.  
APPLICANT: MEYERSON, MATTHEW  
APPLICANT: PAEZ, JUAN GUILHERMO  
APPLICANT: SELLERS, WILLIAM R.  
APPLICANT: SETTLEMEN, JEFFREY E.  
APPLICANT: SORRELLA, NAFFABELA  
TITLE OF INVENTION: METHOD TO DETERMINE RESPONSIVENESS OF CANCER TO  
TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR TARGETING  
FILE REFERENCE: 030258-055147  
CURRENT APPLICATION NUMBER: US/11/294,621  
CURRENT FILING DATE: 2005-12-05  
PRIOR APPLICATION NUMBER: PCT/US05/010645  
PRIOR FILING DATE: 2005-03-31  
PRIOR APPLICATION NUMBER: 60/558,218  
PRIOR FILING DATE: 2004-03-31  
PRIOR APPLICATION NUMBER: 60/561,095  
PRIOR FILING DATE: 2004-04-09  
PRIOR APPLICATION NUMBER: 60/565,753  
PRIOR FILING DATE: 2004-04-27  
PRIOR APPLICATION NUMBER: 60/565,985  
PRIOR FILING DATE: 2004-04-27  
PRIOR APPLICATION NUMBER: 60/574,035  
PRIOR FILING DATE: 2004-05-25  
PRIOR APPLICATION NUMBER: 60/577,916



/ PRIOR FILING DATE: 2004-06-07  
/ PRIOR APPLICATION NUMBER: 60/592,287  
/ PRIOR FILING DATE: 2004-07-29  
/ NUMBER OF SEQ ID NOS: 762  
/ SOFTWARE: Patent Ver. 3.3  
/ SEQ ID NO 70  
/ LENGTH: 20  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-11-294-621-70

Alignment Scores:  
Pred. No.: 926  
Score: 6.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 0.90%  
DB: 7  
Length: 20  
Matches: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-11-294-621-70 (1-20)

Qy 77 Thrsbthrsgrlythr 82  
Db 19 ACTTCACCTCGGCACA 2

RESULT 5  
US-11-317-798-5513  
/ Sequence 5513, Application US/11317798  
/ GENERAL INFORMATION:  
/ APPLICANT: Lofton-Day, Cathy; Model, Fabiani, Sledziewski,  
/ APPLICANT: Andrew; Rujan, Tamas; Lewin, Joern; Discher, Jergen  
/ TITLE OF INVENTION: Methods and nucleic acids for the analysis of colon cell  
/ FILE REFERENCE: 47675-174  
/ CURRENT APPLICATION NUMBER: US/11/317,798  
/ PRIOR FILING DATE: 2005-12-23  
/ PRIOR APPLICATION NUMBER: US 10/603,138  
/ PRIOR FILING DATE: 2003-06-23  
/ PRIOR APPLICATION NUMBER: PCT/US04/20336  
/ PRIOR FILING DATE: 2004-06-23  
/ PRIOR APPLICATION NUMBER: US 10/602,494  
/ PRIOR FILING DATE: 2003-06-23  
/ PRIOR APPLICATION NUMBER: EP 04090175.3  
/ PRIOR FILING DATE: 2004-05-06  
/ PRIOR APPLICATION NUMBER: EP 04090072.2  
/ PRIOR FILING DATE: 2004-02-27  
/ NUMBER OF SEQ ID NOS: 14624  
/ SEQ ID NO 5513  
/ LENGTH: 20  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE: bisulfite treated:  
/ OTHER INFORMATION: nucleic acid for analysis of methylation status of SEQ ID NO: 45  
US-11-317-798-5513

Alignment Scores:  
Pred. No.: 926  
Score: 6.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 0.90%  
DB: 7  
Length: 20  
Matches: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-11-317-798-5513 (1-20)

Qy 394 ValArgSerPheSer 399  
Db 1 GTGACCTTCCTTTTCG 18

RESULT 6  
US-60-742-219-4800  
/ Sequence 4800, Application US/60742219  
/ GENERAL INFORMATION:

/ APPLICANT: Belouchi, Abdelmajid  
/ APPLICANT: Raelson, John Verner  
/ APPLICANT: Bradley, Walter Edward  
/ APPLICANT: Peguin, Bruno  
/ APPLICANT: Nguyen-Huu, Quynh  
/ APPLICANT: Croteau, Pascal  
/ APPLICANT: Allard, Rene  
/ APPLICANT: Little, Randall David  
/ APPLICANT: Ketch, Tim  
/ APPLICANT: Cousineau, Johanne  
/ APPLICANT: Berdevegh, Paul Van  
/ APPLICANT: Segal, Jonathan  
/ TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis  
/ FILE REFERENCE: 306522-2000  
/ CURRENT APPLICATION NUMBER: US/60/742,219  
/ PRIOR FILING DATE: 2005-12-05  
/ NUMBER OF SEQ ID NOS: 7303  
/ SOFTWARE: Patent version 3.3  
/ SEQ ID NO 4800  
/ LENGTH: 21  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-60-742-219-4800

Alignment Scores:  
Pred. No.: 967  
Score: 6.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 0.90%  
DB: 8  
Length: 21  
Matches: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-60-742-219-4800 (1-21)

Qy 243 SerSerLeuGluProGln 248  
Db 3 TCCTCCTTGAGCCACAG 20

RESULT 7  
US-11-130-645B-8449  
/ Sequence 8449, Application US/1130645B  
/ GENERAL INFORMATION:  
/ APPLICANT: ROSETTA GENOMICS LTD  
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF  
/ FILE REFERENCE: 06087,0202,CPUS13  
/ CURRENT APPLICATION NUMBER: US/11/130,645B  
/ PRIOR FILING DATE: 2005-05-16  
/ NUMBER OF SEQ ID NOS: 76016  
/ SOFTWARE: Patent version 3.3  
/ SEQ ID NO 8449  
/ LENGTH: 22  
/ TYPE: RNA  
/ ORGANISM: Homo sapiens  
US-11-130-645B-8449

Alignment Scores:  
Pred. No.: 1,016+03  
Score: 6.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 0.90%  
DB: 7  
Length: 22  
Matches: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-048-046-2 (1-664) x US-11-130-645B-8449 (1-22)

Qy 3 ArgProGluGluGlyLe 8  
Db 4 AGCCGAGGAGCGGAG 21

RESULT 8  
US-11-130-645B-10537  
/ Sequence 10537, Application US/1130645B  
/ GENERAL INFORMATION:

```

/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 10537
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-10537

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-10537 (1-22)

Qy 195 ProSerProAlaGlyArg 200
Db 5 CCCUCUCUCUGUGGCGA 22

RESULT 9
US-11-130-645B-10712/c
/ Sequence 10712, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 10712
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-10712

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-10712 (1-22)

Qy 452 GlyAlaProGlnAlaLeu 457
Db 22 GGGCGTCCCCAGGCGCTC 5

RESULT 10
US-11-130-645B-13922
/ Sequence 13922, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 13922
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens

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US-11-130-645B-13922

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-13922 (1-22)

Qy 368 AspLysSerArgSergL 373
Db 5 GAUAAGUCAGGUCUGAA 22

RESULT 11
US-11-130-645B-13924
/ Sequence 13924, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 13924
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-13924

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-13924 (1-22)

Qy 368 AspLysSerArgSergL 373
Db 5 GAUAAGUCAGGUCUGAA 22

RESULT 12
US-11-130-645B-13926
/ Sequence 13926, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRONAS AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760616
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 13926
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-130-645B-13926

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
Gaps: 0
DB: 0

US-10-048-046-2 (1-664) x US-11-130-645B-13926 (1-22)

```

Qy 368 Applysergsergju 373  
 |||||  
 Db 5 GAUAGUCAGGUCUGA 22

## RESULT 13

US-11-130-645B-16045  
 / Sequence 16045, Application US/11130645B  
 / GENERAL INFORMATION:  
 / APPLICANT: ROSETTA GENOMICS LTD  
 / TITLE OF INVENTION: MICRONAS AND USBS THEREOF  
 / FILE REFERENCE: 06087.0202.CPUS13  
 / CURRENT APPLICATION NUMBER: US/11/130,645B  
 / CURRENT FILING DATE: 2005-05-16  
 / NUMBER OF SEQ ID NOS: 760616  
 / SOFTWARE: PatentIn version 3.3  
 / SEQ ID NO 16045  
 / LENGTH: 22  
 / TYPE: RNA  
 / ORGANISM: Homo sapiens  
 / OTHER INFORMATION: US-11-130-645B-16045

## Alignment Scores:

Pred. No.:	1.01e+03	Length:	22
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	7	Gaps:	0

US-10-048-046-2 (1-664) x US-11-130-645B-16045 (1-22)

Qy 161 ValProProserBerPro 166  
 |||||  
 Db 5 GUCCUCCUCCAGUCGA 22

## RESULT 14

US-10-515-051-78  
 / Sequence 78, Application US/10515051  
 / GENERAL INFORMATION:  
 / APPLICANT: OHNO, Ryozo  
 / APPLICANT: TSURUO, Takashi  
 / APPLICANT: NAKAMURA, Yusuke  
 / TITLE OF INVENTION: METHOD FOR JUDGING SENSIBILITY TO IMATINIB  
 / FILE REFERENCE: 0760-0342PUS1  
 / CURRENT APPLICATION NUMBER: US/10/515,051  
 / CURRENT FILING DATE: 2004-11-19  
 / PRIOR APPLICATION NUMBER: PCT/JP03/06330  
 / PRIOR FILING DATE: 2003-05-21  
 / NUMBER OF SEQ ID NOS: 154  
 / SEQ ID NO 78  
 / LENGTH: 23  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Oligonucleotide reverse primer used for amplifying human CTS6 CDN  
 / OTHER INFORMATION: A  
 / US-10-515-051-78

## Alignment Scores:

Pred. No.:	1.05e+03	Length:	23
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	6	Gaps:	0

US-10-048-046-2 (1-664) x US-10-515-051-78 (1-23)

Qy 17 GlyArgLeuLeuArgLeu 22  
 |||||  
 Db 4 GGACGTTTATTAAAGCTC 21

## RESULT 15

US-11-067-260-59  
 / Sequence 59, Application US/11067260  
 / GENERAL INFORMATION:  
 / APPLICANT: Arico, Maria  
 / TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS  
 / FILE REFERENCE: 223002099501  
 / CURRENT APPLICATION NUMBER: US/11/067,260  
 / CURRENT FILING DATE: 2005-02-25  
 / PRIOR APPLICATION NUMBER: 10/220,480  
 / PRIOR FILING DATE: 2002-08-28  
 / PRIOR APPLICATION NUMBER: PCT/IB01/00420  
 / PRIOR FILING DATE: 2001-02-28  
 / NUMBER OF SEQ ID NOS: 121  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 59  
 / LENGTH: 25  
 / TYPE: DNA  
 / ORGANISM: Artificial  
 / FEATURE:  
 / OTHER INFORMATION: fu (961 ) -741 (MC58) -His Pwd  
 / US-11-067-260-59

## Alignment Scores:

Pred. No.:	1.13e+03	Length:	25
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.90%	Indels:	0
DB:	7	Gaps:	0

US-10-048-046-2 (1-664) x US-11-067-260-59 (1-25)

Qy 207 Glyserglyglyglygly 212  
 |||||

Db 4 GGATCCGAGGCGGTGT 21

Search completed: January 12, 2006, 13:31:58  
 Job time : 130 secs